

<!--StartFragment-->RESULT 1

HAL2_YEAST

ID HAL2_YEAST STANDARD; PRT; 357 AA.

AC P32179;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) (3'(2'),5-

DE bisphosphonucleoside 3'(2')-phosphohydrolase) (DPNPase) (Halotolerance

DE protein HAL2).

GN Name=HAL2; Synonyms=MET22; OrderedLocusNames=YOL064C;

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=93345455; PubMed=8393782;

RA Glaeser H.-U., Thomas D., Gaxiola R., Montrichard F.,

RA Surdin-Kerjan Y., Serrano R.;

RT "Salt tolerance and methionine biosynthesis in Saccharomyces

RT cerevisiae involve a putative phosphatase gene.";

RL EMBO J. 12:3105-3110(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=97321807; PubMed=9178509;

RX DOI=10.1002/(SICI)1097-0061(199705)13:6<583::AID-YEA111>3.0.CO;2-Y;

RA Tzermia M., Katsoulou C., Alexandraki D.;

RT "Sequence analysis of a 33.2 kb segment from the left arm of yeast

RT chromosome XV reveals eight known genes and ten new open reading

RT frames including homologues of ABC transporters, inositol phosphatases

RT and human expressed sequence tags.";

RL Yeast 13:583-589(1997).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=S288c / FY1679;

RX MEDLINE=97313270; PubMed=9169874;

RA Dujon B., Albermann K., Aldea M., Alexandraki D., Ansorge W.,

RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,

RA Boyer J., Camasses A., Casamayor A., Casas C., Cheret G.,

RA Cziepluch C., Daignan-Fornier B., Dang D.V., de Haan M., Delius H.,

RA Durand P., Fairhead C., Feldmann H., Gaillon L., Galisson F.,

RA Gamo F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,

RA Habbig B., Hand N.J., Hani J., Hattenhorst U., Hebling U.,

RA Hernando Y., Herrero E., Heumann K., Hiesel R., Hilger F., Hofmann B.,

RA Hollenberg C.P., Hughes B., Jauniaux J.-C., Kalogeropoulos A.,

RA Katsoulou C., Kordes E., Lafuente M.J., Landt O., Louis E.J.,

RA Maarse A.C., Madania A., Mannhaupt G., Marck C., Martin R.P.,

RA Mewes H.-W., Michaux G., Paces V., Parle-McDermott A.G., Pearson B.M.,

RA Perrin A., Pettersson B., Poch O., Pohl T.M., Poiray R.,

RA Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Rechmann S.,

RA Schwager C., Schweizer M., Sor F., Sterky F., Tarassov I.A.,

RA Teodoru C., Tettelin H., Thierry A., Tobiasch E., Tzermia M.,

RA Uhlen M., Unseld M., Valens M., Vandenbol M., Vetter I., Vlcek C.,

RA Voet M., Volckaert G., Voss H., Wambutt R., Wedler H., Wiemann S.,

RA Winsor B., Wolfe K.H., Zollner A., Zumstein E., Kleine K.;

RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.";

RL Nature 387:98-102(1997).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) IN COMPLEX WITH MAGNESIUM IONS

RP AND AMP.

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RX  MEDLINE=20123982; PubMed=10656801; DOI=10.1006/jmbi.1999.3408;
RA  Albert A., Yenush L., Gil-Mascarell M.R., Rodriguez P.L., Patel S.,
RA  Martinez-Ripoll M., Blundell T.L., Serrano R.;
RT  "X-ray structure of yeast Hal2p, a major target of lithium and sodium
RT  toxicity, and identification of framework interactions determining
RT  cation sensitivity.";
RL  J. Mol. Biol. 295:927-938(2000).
CC  -!- FUNCTION: Converts adenosine 3'-phosphate 5'-phosphosulfate (PAPS)
CC      to adenosine 5'-phosphosulfate (APS) and 3'(2')-phosphoadenosine
CC      5'- phosphate (PAP) to AMP. Regulates the flux of sulfur in the
CC      sulfur-activation pathway by converting PAPS to APS. Involved in
CC      salt tolerance. Confers resistance to lithium.
CC  -!- CATALYTIC ACTIVITY: Adenosine 3',5'-bisphosphate + H(2)O =
CC      adenosine 5'-phosphate + phosphate.
CC  -!- COFACTOR: Magnesium.
CC  -!- INDUCTION: By salt stress.
CC  -!- SIMILARITY: Belongs to the inositol monophosphatase family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; X72847; CAA51361.1; -; Genomic_DNA.
DR  EMBL; Z74806; CAA99074.1; -; Genomic_DNA.
DR  PIR; S35318; S35318.
DR  PDB; 1K9Y; X-ray; A=1-357.
DR  PDB; 1K9Z; X-ray; A=1-357.
DR  PDB; 1KA0; X-ray; A=1-357.
DR  PDB; 1KA1; X-ray; A=1-357.
DR  PDB; 1QGX; X-ray; A=1-357.
DR  GermOnline; 143487; -.
DR  Ensembl; YOL064C; Saccharomyces cerevisiae.
DR  SGD; S000005425; MET22.
DR  GO; GO:0005737; C:cytoplasm; IDA.
DR  GO; GO:0008441; F:3'(2'),5'-bisphosphate nucleotidase activity; TAS.
DR  GO; GO:0042538; P:hyperosmotic salinity response; TAS.
DR  GO; GO:0009086; P:methionine biosynthesis; TAS.
DR  GO; GO:0000103; P:sulfate assimilation; TAS.
DR  InterPro; IPR006239; Bisphos_HAL2.
DR  InterPro; IPR000760; Inositol_P.
DR  Pfam; PF00459; Inositol_P; 1.
DR  PRINTS; PR00378; INOSPHPTASE.
DR  ProDom; PD023420; Inositol_P; 1.
DR  TIGRFAMs; TIGR01330; bisphos_HAL2; 1.
DR  PROSITE; PS00629; IMP_1; 1.
DR  PROSITE; PS00630; IMP_2; 1.
KW  3D-structure; Complete proteome; Hydrolase; Lithium; Magnesium;
KW  Metal-binding.
FT  METAL          72      72      Magnesium 2.
FT  METAL          142     142     Magnesium 1 and 2.
FT  METAL          145     145     Magnesium 1.
FT  METAL          294     294     Magnesium 1.
FT  HELIX           4      30
FT  TURN           31      34
FT  STRAND          36      38
FT  TURN           40      41
FT  STRAND          44      46
FT  HELIX           47      63
FT  TURN           65      66

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| | | | |
|----|----------|---------|-----------------------------------|
| FT | STRAND | 69 | 71 |
| FT | TURN | 76 | 77 |
| FT | HELIX | 80 | 100 |
| FT | TURN | 104 | 105 |
| FT | HELIX | 118 | 126 |
| FT | TURN | 127 | 128 |
| FT | STRAND | 129 | 129 |
| FT | STRAND | 137 | 145 |
| FT | TURN | 146 | 146 |
| FT | HELIX | 147 | 151 |
| FT | TURN | 152 | 153 |
| FT | STRAND | 157 | 164 |
| FT | TURN | 165 | 166 |
| FT | STRAND | 167 | 175 |
| FT | TURN | 176 | 177 |
| FT | HELIX | 180 | 183 |
| FT | TURN | 184 | 184 |
| FT | TURN | 189 | 190 |
| FT | HELIX | 191 | 194 |
| FT | STRAND | 196 | 201 |
| FT | TURN | 202 | 203 |
| FT | STRAND | 206 | 210 |
| FT | TURN | 211 | 213 |
| FT | STRAND | 218 | 219 |
| FT | HELIX | 228 | 230 |
| FT | STRAND | 232 | 235 |
| FT | TURN | 239 | 241 |
| FT | HELIX | 244 | 253 |
| FT | TURN | 254 | 255 |
| FT | STRAND | 258 | 261 |
| FT | TURN | 265 | 265 |
| FT | HELIX | 266 | 273 |
| FT | TURN | 274 | 274 |
| FT | STRAND | 278 | 281 |
| FT | TURN | 286 | 287 |
| FT | STRAND | 291 | 291 |
| FT | HELIX | 292 | 294 |
| FT | TURN | 295 | 295 |
| FT | HELIX | 296 | 304 |
| FT | TURN | 305 | 306 |
| FT | STRAND | 308 | 310 |
| FT | STRAND | 317 | 317 |
| FT | TURN | 320 | 321 |
| FT | STRAND | 325 | 325 |
| FT | STRAND | 331 | 334 |
| FT | HELIX | 338 | 353 |
| FT | TURN | 354 | 354 |
| SQ | SEQUENCE | 357 AA; | 39149 MW; AB2E5F90B285702B CRC64; |

Query Match 100.0%; Score 1838; DB 1; Length 357;
 Best Local Similarity 100.0%; Pred. No. 2.8e-141;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|----|---|-----|
| Qy | 1 | ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIAK | 60 |
| | | | |
| Db | 2 | ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIAK | 61 |
| Qy | 61 | SNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDV | 120 |
| | | | |
| Db | 62 | SNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDV | 121 |

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Qy      121 RQIIDFGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLS 180
        |||
Db      122 RQIIDFGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLS 181
        |||
Qy      181 SYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGH 240
        |||
Db      182 SYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGH 241
        |||
Qy      241 SSHDEQTAIKNKLNISKSLHLD SQAKYCLLALGLADVYLRLPIKLSYQEKIWDHAAGNVI 300
        |||
Db      242 SSHDEQTAIKNKLNISKSLHLD SQAKYCLLALGLADVYLRLPIKLSYQEKIWDHAAGNVI 301
        |||
Qy      301 VHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSRNA 356
        |||
Db      302 VHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSRNA 357
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